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Genetic structure of *Hylesia metabus* (Lepidoptera: Saturniidae): Moths responsible for lepidopteran outbreaks in French Guiana and Venezuela

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Introduction: The genus *Hylesia* Hübner (Lepidoptera Saturniidae) involves moths of human health importance in South America, inducing epidemic outbreaks of lepidopterism, a puriginous dermatitis caused by the urticating properties of the females' abdominal hairs. The genus includes about 110 species in South America, several species having been clearly identified as responsible for health problems. The species *H. metabus* is considered as widespread at low elevation in South America. Furthermore, outbreaks of *H. metabus* have been reported in Atlantic coastal countries such as Venezuela, Guyana, Suriname and French Guiana since the last century. In spite of their sanitary and economics importance these moths have been poorly studied, and their ecology and systematics remain unclear.

Methods: In order to evaluate genetic differentiation among populations of *Hylesia metabus*, specific microsatellite primers have been developed on moths sampled during outbreak events. Moths from 20 sampling locations throughout the outbreak areas in French Guiana and Venezuela were analyzed at 7 microsatellite loci.

Results/Conclusion: We found significant genetic population structure as evidenced by Bayesian-based and Multivariate analysis. Our data support the hypothesis of multiple highly differentiated populations . Interestingly only few of them seem to be involved in lepidopterism events occurring in French Guiana and in Venezuela. These findings emphasize the utility of molecular approaches for identifying population structure and connectivity. Such approaches constitute useful tools for understanding outbreak patterns.